What is claimed is:

1. An isolated nucleic acid molecule selected from SEQ ID NO:1-42, and regulatory sequences associated therewith.

2. The nucleic acid molecule of claim 1, wherein said associated regulatory sequences contain CpG-rich regions.

3. The nucleic acid molecule of claim 2, wherein the state of methylation of the CpG-rich regions is determinative of the presence of a cellular proliferative disorder in a subject from which the nucleic acid molecule is isolated.

4. The nucleic acid molecule of claim 2, wherein hypermethylation of said CpG islands is indicative of the presence of a cellular proliferative disorder in a subject from which said nucleic acid is isolated.

5. The nucleic acid molecule of claim 1, wherein the molecule is selected from SEQ I D NO:39-42.

6. A substantially purified polypeptide encoded by a polynucleotide selected from SEQ ID NO:39-42.

7. A method for detecting a cellular proliferative disorder in a subject comprising:

a) contacting a nucleic acid-containing specimen from the subject with an agent that provides a determination of the methylation state of at least one gene or associated regulatory region of the gene selected from MICP1-42 of Table 1 and combinations thereof; and

b) identifying aberrant methylation of regions of the gene or regulatory region, wherein aberrant methylation is identified as being different when compared to

the same regions of the gene or associated regulatory region in a subject not having said cellular proliferative, thereby detecting a cellular proliferative disorder in the subject.

8. The method of claim 7, wherein the regions of said gene are contained within CpG rich regions.

9. The method of claim 7, wherein the gene is SEQ ID NO:39, 40, 41 or 42.

10. The method of claim 7, wherein aberrant methylation comprises hypermethylation when compared to the same regions of the gene or associated regulatory regions in a subject not having the cellular proliferative disorder.

11. The method of claim 10, wherein the regions comprise regulatory regions of the gene.

12. The method of claim 7, wherein the agent is a pair of primers that hybridize with a target sequence in the gene or associated regulatory region of the gene.

13. The method of claim 7, wherein the nucleic acid-containing specimen comprises a tissue selected from the group consisting of brain, colon, urogenital, lung, renal, prostate, pancreas, liver, esophagus, stomach, hematopoietic, breast, thymus, testis, ovarian, and uterine.

14. The method of claim 7, wherein the nucleic acid-containing specimen is selected from the group consisting of serum, urine, saliva, blood, duodenal fluid, pancreatic fluid, cerebrospinal fluid, pleural fluid, ascites fluid, sputum, stool, and biopsy sample.

15. The method of claim 11, wherein said cellular proliferative disorder is selected from the group consisting of low grade astrocytoma, anaplastic astrocytoma, glioblastoma, medulloblastoma, gastric cancer, colorectal cancer, colorectal adenoma, acute myelogenous leukemia, lung cancer, renal cancer, leukemia, breast cancer, prostate cancer, endometrial cancer and neuroblastoma.

16. A kit useful for the detection of a cellular proliferative disorder in a subject comprising:

a) carrier means compartmentalized to receive a sample therein;

b) one or more containers comprising a first container containing a reagent which modifies unmethylated cytosine and a second container containing primers for amplification of a CpG-containing nucleic acid, wherein the primer hybridizes with a target polynucleotide sequence having the sequence selected from SEQ ID NO:1-42.

17. The kit of claim 16, further comprising a third container containing a methylation sensitive restriction endonuclease.

18. The kit of claim 16, wherein said modifying reagent is bisulfite.

19. The kit of claim 16, wherein the primer hybridizes with a target polynucleotide sequence having a sequence as set forth in SEQ ID NO:39, 40, 41 or 42.

20. Isolated oligonucleotide primer(s) for detection of a methylated CpG-containing nucleic acid wherein the primer hybridizes with a target polynucleotide sequence having the sequence selected from the group consisting of SEQ ID NO:1-42.

21. Isolated oligonucleotide primer pairs selected from SEQ ID NO:43-105.